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Attorney's Docket No.: 10454-019001

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

2621

Applicant : Kemal Sonmez, et al
Serial No. : 10/004,580
Filed : December 3, 2001
Title : DATA RELATIONSHIP MODEL

Art Unit : 2621
Examiner : Unknown

Commissioner for Patents
Washington, D.C. 20231

INFORMATION DISCLOSURE STATEMENT

Applicant submits the references listed on the attached form PTO-1449, copies of which are enclosed.

This statement is being filed before the receipt of a first Office action on the merits.

Please apply any charges or credits to Deposit Account No. 06-1050.

Respectfully submitted,

Date: 4/4/2

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I hereby certify under 37 CFR §1.8(a) that this correspondence is being deposited with the United States Postal Service as first class mail with sufficient postage on the date indicated below and is addressed to the Commissioner for Patents, Washington, D.C. 20231.

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Substitute Form PTO-1449 (Modified)	U.S. Department of Commerce Patent and Trademark Office	Attorney's Docket No. 10454-019001	Application No. 10/004,580
Information Disclosure Statement by Applicant (Use several sheets if necessary)		Applicant Kemal Sonmez, et al	
37 CFR 1.98(b))		Filing Date December 3, 2001	Group Art Unit 2621

U.S. Patent Documents

Examiner Initial	Desig. ID	Patent Number	Issue Date	Patentee	Class	Subclass	Filing Date If Appropriate
	AA	6,128,587	10/03/2000	Sjolander			
	AB						

Foreign Patent Documents or Published Foreign Patent Applications

Examiner Initial	Desig. ID	Document Number	Publication Date	Country or Patent Office	Class	Subclass	Translation Yes	Translation No
	AC							
	AD							

Other Documents (include Author, Title, Date, and Place of Publication)

Examiner Initial	Desig. ID	Document
	AE	Baldi, P. et al., "Hidden Markov Models of Biological Primary Sequence Information", *Proc. Natl. Acad. Sci. USA*, Vol. 91, pp. 1059-1063; February 1994.
	AF	Barrett, C. et al. "Scoring Hidden Markov Models", *CABIOS*, Vol. 13, No. 2, pp. 191-199; 1997.
	AG	Brakch, N. et al. "Favourable Side-Chain Orientation of Cleavage Site Dibasic Residues of Prohormone in Proteolytic Processing by Prohormone Convertase 1/3", *Eur. J. biochem.* Vol. 267, pp. 1626-1632; 2000.
	AH	Brown, M. et al., "Using Dirichlet Mixture Priors to Derive Hidden Markov Models for Protein Families", *Proc. of First Int. Conf. on Intelligent Systems for Molecular Biology* , pages 47--55, Menlo Park, CA, July 1993. AAAI/MIT Press.
	AI	Bucher, P. et al., ""A Flexible Motif Search Technique based on Generalized Profiles", *Computers and Chemistry*, Vol. 20 pp. 3-24. January 1996.
	AJ	Chesneau, V. et al., "N-Arginine Dibasic Convertase (NRD Convertase): A Newcomer to the Family of Processing Endopeptidases", *Biochimie* Vol. 76, pp. 234-240; Paris, March 1994.
	AK	Chou, K-C. et al., "Studies on the Specificity of HIV Protease: An Application of Markov Chain Theory", *Journal of Protein Chemistry*, Vol. 12, No. 6, pp. 709-724; 1993.
	AL	Chou, K-C., "Prediction of Human Immunodeficiency Virus Protease Cleavage Sites in Protein", *Analytical Biochemistry* Vol. 233, pp. 1-14; 1996.
	AM	Chou, K-C. et al., "Predicting Human Immunodeficiency Virus Protease Cleavage Sites in Proteins by a Discriminant Function Method", *Proteins:Structure, Function, and Genetics* Vol. 24, pp. 51-72; 1996.
	AN	Eddy, SR., "Hidden Markov Models", *Current Opinion in Structural Biology*, Vol. 6, pp. 361-365, 1996.
	AO	Eddy, SR., "Profile Hidden Markov Models", *Bioinformatics, Vol. 14, review of HMMs* 1998.
	AP	Eddy, SR. et al., "Maximum Discrimination Hidden Markov Models of Sequence Consensus", *J. Computational Biology* Vol. 2 pp. 9-23, 1994.
	AQ	Eddy, SR., "Multiple Alignment Using Hidden Markov Models", *Proc. Third Int. Conf. Intelligent Systems for Molecular Biology,. AAAI Press*, Menlo Park. pp. 114-120. PostScript; 1995.

Examiner Signature	Date Considered

EXAMINER: Initials citation considered. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

Substitute Form PTO-1449 (Modified)	U.S. Department of Commerce Patent and Trademark Office	Attorney's Docket No. 10454-019001	Application No. 10/004,588
Information Disclosure Statement by Applicant (Use several sheets if necessary) (37 CFR 1.98(b))		Applicant Kemal Sonmez, et al	
		Filing Date December 3, 2001	Group Art Unit 2621

Other Documents (include Author, Title, Date, and Place of Publication)

Examiner Initial	Desig. ID	Document
	AR	Grate, L, et al., "Tutorial: Stochastic Modeling Techniques: Understanding and Using Hidden Markov Models" University of California, Santa Cruz, CA, pp 1-34, June 1996.
	AS	Grice, JA. Et al., "Reduced Space Sequence Alignment", *CABIOS*, Vol. 13, pp. 45-53, 1997.
	AT	Grundy, WN., et al. ""Meta-MEME: Motif-Based Hidden Markov Models of Protein Families", to appear in *Computer Applications in the Biosciences*, 1997.
	AU	Hughey, R. et al., "Hidden Markov Models for Sequence Analysis: Extension and Analysis of the Basic Method", Reprint *CABIOS* Vol. 12, pp. 95-107, 1996.
	AV	Hughey, R. et al., "SAM : Sequence Alignment and Modeling Software System", *Technical Report UCSC-CRL-96-22*, University of California, Santa Cruz, CA, July 1998..
	AW	Hughey, R., "Massively Parallel Biosequence Analysis.", *Technical Report UCSC-CRL-93-14*, University of California, Santa Cruz, CA, April 1993.
	AX	Jagla, B. et al., "Adaptive Encoding Neural Networks for the Recognition of Human Signal Peptide Cleavage Sites" *BIO, Vol. 16*, No. 3, March 2000.
	AY	Karchin, R. et al., "Weighting Hidden Markov Models for Maximum Discrimination", *Bioinformatics*, Vol. 14, pp. 772-782, 1998.
	AZ	Karchin, R., "Hidden Markov Models and Protein Sequence Analysis" from http://www.cse.ucsc.edu/research/compbio/ismb99.handouts//KK185FP.html printed from website March 14, 2002.
	AAA	Karplus, K. et al., "Hidden Markov Models for Detecting Remote Protein Homologies", *BIO Informatics*, Vol. 14, No. 10, pp. 846-856; October 1998.
	ABB	Karplus, K. et al., "Predicting Protein Structure Using Hidden Markov Models", *Proteins:Structure, Function, and Genetic*, Suppl., pp. 134-139; September 1997.
	ACC	Krogh, A. et al., "Hidden Markov Models in Computational Biology. Applications to Protein Modeling", *J. Mol. Biol.* Vol. 235, pp. 1501-1531; February 1994.
	ADD	Krogh, A. et al., Predicting Transmembrane Protein Topology with a Hidden Markov Model: Application to Complete Genomes" *Journal of Molecular Biology* Vol 305, No. 3, pp.567-580; 2001.
	AEE	Ladunga, I., "Large-Scale Predictions of Secretory Proteins from Mammalian genomic and EST sequences" *Analytical Biotechnology*, pp. 13-18; 2000.
	AFF	Lockless, SW. et al. "Evolutionarily Conserved Pathways of Energetic Connectivity in Protein Families", *Science* Vol. 286, pp. 295-299; October 1999.
	AGG	McClure, MA.et al., "Parameterization studes for the SAM and HMMER methods of hidden Markov model generation", *Proc. Fourth Int. Conf. Intelligent Systems for Molecular Biology*, pp. 155-164, UNLV, Las Vegas.
	AHH	Nielsen, H.et al., "Identification of Prokaryotic and Eukaryotic Signal Peptides and Prediction of Cleavage Sites", *Protein Engineering* Vol. 10, No 1, pp.1-6; January 1997.
	AII	Nielsen, H. et al. "Prediction of Signal Peptides and Signal Anchors by a Hidden Markov Model", *American Association for Artificial Intelligence ISMB*, pp. 122-130; 1998.
	AJJ	Nielsen, H. et al. "Machine Learning Approaches for the Prediction of Signal Peptides and Other Protein Sorting Signals", *Protein Engineering* Vol. 12, No. 1, pp. 3-9; January 1999.
	AKK	Paracel, "Hidden Markov Model", from http://paracel.com/publications/hmm_white_paper.html printed from website March 14, 2002.

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Information Disclosure Statement by Applicant (Use several sheets if necessary) (37 CFR 1.98(b))		Applicant Kemal Sonmez, et al	
		Filing Date December 3, 2001	Group Art Unit 2621

Other Documents (include Author, Title, Date, and Place of Publication)		
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	ALL	Rabiner, LR., "A Tutorial on Hidden Markov Models and Selected Applications in Speech Recognition", *Proceedings of the IEEE*, Vol. 77, No 2, pp.257-186; February 1989.
	AMM	Rholam, M. et al., "Role of Amino Acid Sequences Flanking Dibasic Cleavage Sites in Precursor Proteolytic Processing. The Importance of the First Residue C-terminal of the cleavage site", *Eur. J. Biochem* .Vol. 227, pp. 707-714; February 1995.
	ANN	Tarnas, C. et al., "Reduced space hidden Markov model training", *Bioinformatics,* Vol. 14. pp. 401-406, 1998.
	AOO	UCSC Comp. Biol. Group, "Sequence Alignment and Modeling System" from http://www.cse.ucsc.edu/research/compbio/sam.html printed from website March 14, 2002.

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